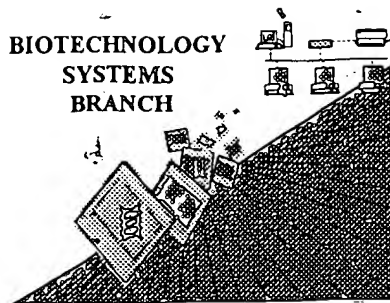# RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09|964,824_

Source: _01PE_

Date Processed by STIC: _10|18|01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09 1964, 824_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
   prevent "wrapping."

2 ____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
   Numbering   use **space characters**, instead.

4 ____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please
   ensure your subsequent submission is saved in ASCII text.**

5 ____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
   each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
   residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
   the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
   Artificial or Unknown sequences.**

7 ____Skipped Sequences   Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped

   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____Skipped Sequences   Sequence(s)_____ missing. If **intentional**, please insert the following lines for each skipped sequence.
   (NEW RULES)   <210> sequence id number
   <400> sequence id number
   000

9 ✓__Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
   is Artificial Sequence

11 ____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
   "Unknown." Please explain source of genetic material in <220> to <223> section.
   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

OIPE

RAW SEQUENCE LISTING   DATE: 10/18/2001
PATENT APPLICATION: **US/09/964,824**   TIME: 10:29:48

Input Set : N:\EBONY'S\ES.txt

Does Not Comply

Output Set: N:\CRF3\10182001\I964824.raw

Corrected Diskette Needed

```
   3 <110> APPLICANT: Horrigan, Stephen
   5 <120> TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
Signature Gene
   6       Sets
   8 <130> FILE REFERENCE: 689290-73
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/964,824
C--> 10 <141> CURRENT FILING DATE: 2001-09-27
  10 <150> PRIOR APPLICATION NUMBER: US/60/236,033
  11 <151> PRIOR FILING DATE: 2000-09-28
  13 <150> PRIOR APPLICATION NUMBER: US/60/236,032
  14 <151> PRIOR FILING DATE: 2000-09-28
  16 <150> PRIOR APPLICATION NUMBER: US/60/236,028
  17 <151> PRIOR FILING DATE: 2000-09-28
  19 <160> NUMBER OF SEQ ID NOS: 583
  21 <170> SOFTWARE: PatentIn version 3.0
  23 <210> SEQ ID NO: 1
  24 <211> LENGTH: 521
  25 <212> TYPE: DNA
  26 <213> ORGANISM: Homo sapiens
  28 <220> FEATURE:
  29 <221> NAME/KEY: misc_feature
  30 <223> OTHER INFORMATION: n=a,t,g or c
  33 <400> SEQUENCE: 1
  34 gtaatatgga attagaaaca atttggcttt ttagagctga aactagaaac aacacatcca     60
  36 ggaacagtag acttctattg tcttcaatcc ctaatgtcct agtgagtatg taccctatgg    120
  38 agaaggcaga aatgacgtgg accaggactc cttacatgga gagtgtttta aaggcagttt    180
  40 ttaaaaagcc cattttgtga aagaaccag aaggctcgta attgctgtct gcactgtggt     240
W--> 42 ttctcctggg ggttggggag gggagtggat taaataaaaa gtttagaagg ccatagnata    300
  44 aatatcgaaa tagtatgaat tttaatatat acttttaaag gggttaggca atgatgaaaa    360
  46 gatatgactg ctttcctttc atttctcatt aaattaaaat tcccacaaaa gtgcatggca    420
  48 tcttttttgaa acactgctaa ttttaaagtt tgggaaggtt tatcttcata gccacaatct    480
W--> 50 ttgcnaaagc cttggtaccg gnaacaaggc tccagtctgc c                        521
  53 <210> SEQ ID NO: 2
  54 <211> LENGTH: 481
  55 <212> TYPE: DNA
  56 <213> ORGANISM: Homo sapiens
  58 <400> SEQUENCE: 2
  59 ataaatggtt tatttttaac ataagtaaat ttacaaatca aatgaaaaat gaaaaataca     60
  61 aaagttcatg aatgaaataa aaaagacact ctcaaaatat taaaacctat ggaaagaaaa    120
  63 taagtaatta atgaatgatg tttttgtttc caaatacaat gaagtgattt tttattagag    180
  65 tccttgggaa tcatctaagt tacaatacag aagagaatta aataaatcgt atatgatttt    240
  67 gtaattagac actctatata tcacagttct ttgttaacct gggcatggaa cgtccctata    300
  69 gcatatattt aaaaccatta attttttta aaaaaatttg agacatggtt tgttcttgtt      360
  71 ctctaaatta tgtttcccca tttcccttga atgttctcta ttggccatct tctggaacat    420
  73 taaaaaaaaa tcttgaaaca aattctcttg caatgatacg tatcacataa acttgatatg    480
  75 c                                                                    481
  78 <210> SEQ ID NO: 3
  79 <211> LENGTH: 357
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Handwritten annotations:

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Errors on pp. 1-4, and ↑.

→ Must give location of N. See error summary sheet Item 9

RAW SEQUENCE LISTING   DATE: 10/18/2001
PATENT APPLICATION: US/09/964,824   TIME: 10:29:48

Input Set : N:\EBONY'S\ES.txt
Output Set: N:\CRF3\10182001\I964824.raw

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 80 <212> TYPE: DNA
 81 <213> ORGANISM: Homo sapiens
 83 <400> SEQUENCE: 3
 84 gagcggtgga gggcgtcact gggtttcggc gtctggcaag cgattcagct gtctgctccc       60
 86 tagcagccgg ccttcgggtc gggcgtcttc cccggctact gccgcttcag ttcttccggt      120
 88 gtggccacga gtcgggttgc acttctgtga tccatcctca tcttctaaag atgcatcctg      180
 90 acttatctcc acacttgcac actgaagaat gcaacgtctt gattaacttg cttaaggaat      240
 92 gtcacaaaaa tcacaacatt ctgaaatttt ttgggtattg taatgatgtt gatcgggggt      300
 94 ggagagaatg cctctagagt gatgtacata gagaacagga gcccgagcag ggggcat        357
 97 <210> SEQ ID NO: 4
 98 <211> LENGTH: 1086
 99 <212> TYPE: DNA
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 4
103 cgcagccgcc cgcccgcccg ctcagcgccc ggccccggga tgacggcggc ccaggccgcg       60
105 ggtgaggagg cgccaccagg cgtgcggtcc gtcaaggtgg tcctggtggg cgacggcggc      120
107 tgcgggaaga cgtcgctgct gatggtcttc gccgatgggg ccttcccccga gagctacacc      180
109 cccacggtgt ttgagcggta catggtcaac ctgcaagtga aaggcaaacc tgtgcacctc      240
111 cacatctggg acacagcagg gcaagatgac tatgaccgcc tgcggcccct gttctaccct      300
113 gacgccagcg tcctgctgct ttgcttcgat gtcaccagcc cgaacagctt tgacaacatc      360
115 tttaaccggt ggtacccaga agtgaatcat ttctgcaaga aggtacccat catcgtcgtg      420
117 ggctgcaaga ctgacctgcg caaggacaaa tcactggtga acaagctccg aagaaacgga      480
119 ttggagcctg tgacctacca caggggccag gagatggcga ggtccgtggg cgcggtggcc      540
121 tacctcgagt gctcggctcg gctccatgac aacgtccacg ccgtcttcca ggaggccgcc      600
123 gaggtggccc tcagcagccg cggtcgcaac ttctggcggc ggattaccca gggcttttgc      660
125 gtggtgacct gagcggctcg gggcgtccca gcgacgcggg aagggggcagg gcgctgacct      720
127 gctgctgagc tggctgggct ggacccggtc cctaggctgt gaccgccgaa ctccactgca      780
129 acagacgggc gccaccaaag ccaggccctg aggcctggga gtcctggact gagaaagggg      840
131 gttcctgggc ccacctgctc tgtgtagggc tcgtcctgcg gtgcccgaga atcactcgct      900
133 aaccccctatg cccggtcccg daccgacatc ctggagccgc ctgtgcagcc tgatgccccc      960
135 tcgtggctgc tcccagggct gcacctgcca ggacctaatg ttcttaggtc cctctggcca     1020
137 gaacccacac ccggcccctt cccacctgtc atactggtaa ctgtaacaag aaaaacgaca     1080
139 tcactt                                                               1086
142 <210> SEQ ID NO: 5
143 <211> LENGTH: 486
144 <212> TYPE: DNA
145 <213> ORGANISM: Homo sapiens
147 <220> FEATURE:
148 <221> NAME/KEY: misc_feature
149 <223> OTHER INFORMATION: n=a,t,g or c
152 <400> SEQUENCE: 5
153 tagcaccatg atcctcgcgc tggagctgtg tgaggagatc gtggtctatg ggatggtcag       60
155 cgacantanc tgcagggaga agagccaccc ctcagtgcct taccactact ttgagaaggg      120
157 ccggctagat gagtgtcaga tgtacctggc acacgagcag gcgccccgaa gcgccaccgc      180
159 ttcatcactg agaaggcggt cttctcccgc tgggccaaga agaggcccat cgtgttcgcc      240
161 catccgtcct ggaggactga gtagcttccg tcgtcctgcc agccgccatg ccgttgcgag      300
163 gcctccggga tgtcccatcc caagccatca cactccacaa aaacatttaa tttatgggat      360
165 cctgcctcct gccacgtgct gggtgggganc ttaaggttcc ttcccacccc attgtgggcg      420
167 acatttggag ccatttttcag gcttccattc cctgagtaat tcatgggcat tttgggggtt      480
```

W--> on line 155
W--> on line 165

Some error (handwritten annotation near lines 144–149)

```
W--> 169 cancca                                                    486
     172 <210> SEQ ID NO: 6
     173 <211> LENGTH: 1515
     174 <212> TYPE: DNA
     175 <213> ORGANISM: Homo sapiens
     177 <400> SEQUENCE: 6
     178 tttttttttt ttttcatcag gtcagagcca aaggaaagct tgaaaaatga agacattagc      60
     180 aggacttgtt ctgggacttg tcatcttgga tgctgctgtg actgccccaa ctctagagtc     120
     182 catcaactat gactcagaaa cctatgatgc caccttagaa gacctggata atttgtacaa     180
     184 ctatgaaaac atacctgttg ataaagttga gattgaaata gccacagtaa tgccttcagg     240
     186 gaacagagag ctcctcactc caccccaca gcctgagaag gcccaggaag aggaagagga     300
     188 ggaggaatct actcccaggc tgattgatgg ctcttctccc caggagcctg aattcacagg     360
     190 ggttctgggg ccacacacaa atgaagactt tccaacctgt ctttggtgta cttgtataag     420
     192 taccaccgtg tactgtgatg accatgaact tgatgctatt cctccgctgc caaagaacac     480
     194 cgcttatttc tattcccgct ttaacagaat taaaaagatc aacaaaaatg actttgcaag     540
     196 cctaagtgat ttaaaaagga ttgatctgac atcaaattta atatctgaga ttgatgaaga     600
     198 tgcattccga aaactgcctc aacttcgaga gcttgtcctg cgtgacaaca aaataaggca     660
     200 gctcccagaa ttgccaacca cttcgacatt tattgatatt agcaacaata gacttggaag     720
     202 gaaagggata aagcaagaag catttaaaga catgtatgat ctccatcatc tgtacctcac     780
     204 tgataacaac ttggaccaca tccctctgcc actcccagaa aatctacgag cccttcacct     840
     206 ccagaataac aacattctgg aaatgcacga agatacgttc tgcaatggta aaaatttgac     900
     208 ttatattcgt aaggcactag aggacattcg attggatgga aaccctatta atctcagcaa     960
     210 aactccacaa gcatacatgt gtctacctcg tctgcctgtt gggagccttg tctaatttca    1020
     212 gataatggtt agcattacga tggctactat aaataaacca ttcttactgc tctcttccaa    1080
     214 aacaaaactc agcatgatac tttgagattg tgttctgaga gatgatatga ctacataaaa    1140
     216 tacaattaaa aatgttataa tataatgaaa atgtagtaat ttaagaaaac accagatgag    1200
     218 ttaggaataa acctataaca tttacaaaaa gagcaaaact aagtgataga aaatatttca    1260
     220 cacatgttct tatagatcat gtatcacttg caagtttttag gagttcatat cctatatcat    1320
     222 ttcaaattaa gtacataata aagtaaaatt ttgaaatgaa cactttaggt atttttgcca    1380
     224 agatttagat gtttttaatt aaacttttct cttcctttt ttttcactaa ggcatgttta    1440
     226 ttcccctaat ccattaaaga gcatgaaaaa aagaataaat gtatttgaaa aaaaaaaaa    1500
     228 aaaaaaaaaa aaaaa                                                   1515
     231 <210> SEQ ID NO: 7
     232 <211> LENGTH: 480
     233 <212> TYPE: DNA
     234 <213> ORGANISM: Homo sapiens
     236 <220> FEATURE:
     237 <221> NAME/KEY: misc_feature
     238 <223> OTHER INFORMATION: n=a,t,g or c
     241 <400> SEQUENCE: 7
     242 gggaagttta ctgggccatc acagactttt gttctagtga ttgtatgtat taggagtcat      60
     244 agcatgccct acggagatct ggattcttat acactaagat gtgtcttaag aatcacagtg     120
     246 cgtgcttcat ccctttattg aagaacagaa aattatgact actctacaag gtggataata     180
     248 ttttggtacc tgtggctggc cacagccctg ttcctcaaag ctgaattgat agatttctct     240
     250 ttgacttcca agacctagca gttataaggc accttgaaat aaattgtttg tgcctggaaa     300
W--> 252 tgcagggagg gcaatagctt tgtaaattgg nttacatttt tctccttgaa tttttctagg     360
     254 gtcctagtgc ttccgaatca tttaatggca ttgtcggata tccttttaca tttcaattgc     420
     256 aatccatgaa attacattta gaagattctt agtacttaac ggtagtcttc ccatgaattt     480
     259 <210> SEQ ID NO: 8
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RAW SEQUENCE LISTING   DATE: 10/18/2001
PATENT APPLICATION: US/09/964,824   TIME: 10:29:48

Input Set : N:\EBONY'S\ES.txt
Output Set: N:\CRF3\10182001\I964824.raw

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260 <211> LENGTH: 416
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <220> FEATURE:
265 <221> NAME/KEY: misc_feature
266 <223> OTHER_INFORMATION: n=a,t,g or c
269 <400> SEQUENCE: 8
W--> 270 atttcagang aagtttatta agaggtttta ggctttaagc atatgtgaaa agcaaaaatt      60
272 acattttaaa gtatataatt tgcattttcc accttctcaa tgccaatgaa atattctagg      120
274 agactctata agataaccaa ttgattttct actactccca aattttaact ttgtaattta      180
276 aagaggaata ggcaaataga gctgctgtgg ttctggttct ccctgcagga tgaagggggc      240
278 ctgcaaaatg tctcctactt ccattctagg tcattcagca aggtgccttc ctctggatgc      300
280 actgtctgta tacttttgcc atgttgcatc acataatgga ttctggccca ccttacacca      360
W--> 282 ttttgactgt cagtaaaaga atggtatggt ggcccatttc ttcntttatt aatagc         416
285 <210> SEQ ID NO: 9
286 <211> LENGTH: 371
287 <212> TYPE: DNA
288 <213> ORGANISM: Homo sapiens
290 <400> SEQUENCE: 9
291 tttgacacgt gaagggttat ttatggttat gatgaccctg tcctgcaacg agggactggc      60
293 agccactact gaggaggagg gtcccatctc tctcctgtcg gctttcaccg aggtcacagc      120
295 cagacgtggg gcaaaggtgt tccctgtcct acccagccat tcctgggcct gccgcctagg      180
297 ggctcacagg gcccaggagt ccccagctca caggccaggg catcaggcca ggcgcgctcg      240
299 gtgcacaccg cacctgtgga ggacctgggt acactcagga gaccaagagc actggcgggt      300
301 caggatggtt ggcgttcagc tcctacgggg tggggagaag tctgtagccg agagcccagc      360
303 cccctcctgc c                                                           371
306 <210> SEQ ID NO: 10
307 <211> LENGTH: 419
308 <212> TYPE: DNA
309 <213> ORGANISM: Homo sapiens
311 <400> SEQUENCE: 10
312 aagtattctg tccctttaat agctttgttt taggggtaac tcccctcgcc ttgtggggag      60
314 gcttaggacg ggcgggtgca atcctcgaag gggagtctca gcgaccatgg gggacaccat      120
316 ccacatgcag gcggtagttg gggcctcggc agcgcctctc tggggtgccg ggggtccctg      180
318 ttgcccctca gtgccctgtg gcgcaagggc tgcagggcc ggctgttacc gctgaggctc        240
320 tggaagatct gagatggagg attctggctc aggagtctca gggagtgcat ctgaagggag      300
322 gtgatattga gggcccggtc aatgaggatc caggtgacag tctcggagca gggcggggtg      360
324 ctgagagagc cctgataggt gatgaaaccg aagattcagg gaacaggagc tccaggctc        419
327 <210> SEQ ID NO: 11
328 <211> LENGTH: 270
329 <212> TYPE: DNA
330 <213> ORGANISM: Homo sapiens
332 <400> SEQUENCE: 11
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335 tgagctgcgg cacgcagagg tgccagccaa ttccgaggag aattgggtcc aatagaaata      120
337 tttacaaata accagggggc aggtgtgccg tgatcgggaa tcgtgaggga actgagtacc      180
339 aggggccct tggctcccaa cagccccagg ccctgggcg gacttggcac aggacccaag         240
341 agggaactgg ggcattgggg ggccggcaga                                       270
344 <210> SEQ ID NO: 12
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/964,824

DATE: 10/18/2001

TIME: 10:29:48

Input Set : **N:\EBONY'S\ES.txt**
Output Set: **N:\CRF3\10182001\I964824.raw**

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345 <211> LENGTH: 255
346 <212> TYPE: DNA
347 <213> ORGANISM: Homo sapiens
349 <400> SEQUENCE: 12
350 tttagtttag caccatttat taagtgatct cagctgttgt tgtagctgct gcgtgtcacc        60
352 gtgttcttaa aacataaaat gctcttccga ttcctcttgt ccaggacaga aggatcttcc       120
354 aggtagcacg ccaacagaac aagagactcc gatgacgcca gcttcaatga tggtgccatc       180
356 cagagaggga gagggtcatg gcacattcaa ccgcggcttc cagaggtttt gaaaaaggag       240
358 cctttggggg cccag                                                        255
361 <210> SEQ ID NO: 13
362 <211> LENGTH: 358
363 <212> TYPE: DNA
364 <213> ORGANISM: Homo sapiens
366 <400> SEQUENCE: 13
367 caggttgaat aaaatttaat tgataatgct ttatattaat attctctttt gcatttaaat        60
369 attatatgaa tactacaagc atccaacaag aaataacctt cataaattag cataatttat       120
371 agcaggaaac ccaaataaac taaacttggc tgcctaaaat aatttgtcta aagggggata       180
373 tgctctttgt aagtatcatg ctgataaaac cataaaaatt cttttagagg aatgaggatt       240
375 aaaatgaaat ttctttatga cacggaaaaa aataataatt tgtctaaaag tgtaaaattt       300
377 taaaagcaaa cattatacac ataaccagca caattatttc catcttaaaa cattggtt         358
380 <210> SEQ ID NO: 14
381 <211> LENGTH: 266
382 <212> TYPE: DNA
383 <213> ORGANISM: Homo sapiens
385 <400> SEQUENCE: 14
386 atggctaatg gtgacacact ttattaattt aaaaacacgc ccttcccaca tagtgcgtga        60
388 ggcatgtgca cattttccta gaaggacatg aatagtgatg tggaggtacg gtggaggtca       120
390 ggcatctaca gggtcattcg aggaggaaca gattcaagct ttcggacgat cagtgttttg       180
392 taaatagcag catcatcaga tctaagacaa cattggacct ggcagggcct tttctttggg       240
394 tggcattaat tactccagat tcagac                                            266
397 <210> SEQ ID NO: 15
398 <211> LENGTH: 287
399 <212> TYPE: DNA
400 <213> ORGANISM: Homo sapiens
402 <400> SEQUENCE: 15
403 aacgtaaaca caaagtctca tttatttttg tctgaagcac acaggagctc actcagcaca        60
405 ataacagtaa gcgaatcata caaatattga gaaaaaatgt tcctatgaat acatacatgt       120
407 atattcttaa gagtagcgat caggagttta acaacaaatg taaagtggtt ttctctaaag       180
409 aatgctttct gacaggcttt tgggttggaa atggacaggt aaatcactgt cacataacag       240
411 gtaagctaag aataacttct gttacccaag tcatttgaac cctgtgg                      287
414 <210> SEQ ID NO: 16
415 <211> LENGTH: 291
416 <212> TYPE: DNA
417 <213> ORGANISM: Homo sapiens
419 <220> FEATURE:
420 <221> NAME/KEY: misc_feature
421 <223> OTHER INFORMATION: n=a,t,g or c
424 <400> SEQUENCE: 16
425 tttttttttt ttcttgtggc cattcccagg tttaattaca aaccgatccg aacatcccat        60
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/964,824**

DATE: 10/18/2001
TIME: 10:29:49

Input Set : **N:\EBONY'S\ES.txt**
Output Set: **N:\CRF3\10182001\I964824.raw**

```
L:10  M:270 C: Current Application Number differs, Replaced Current Application No
L:10  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:42  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:50  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:50  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:155 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:165 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:169 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:427 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:433 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:447 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:459 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:526 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:532 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:556 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:558 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:588 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:612 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:616 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:674 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:680 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:706 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:708 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
```

VERIFICATION SUMMARY   DATE: 10/18/2001
PATENT APPLICATION: US/09/964,824   TIME: 10:29:49

Input Set : **N:\EBONY'S\ES.txt**
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```
L:1184 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1186 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1188 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:1188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1190 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:1190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:1204 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:1214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:1216 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:1216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:1259 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L:1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L:1261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:1279 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:55
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:1297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:56
L:1297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:1339 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:57
L:1339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1341 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:57
L:1341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
L:1394 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:59
L:1394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:1465 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:63
L:1465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1469 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:63
L:1469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:1485 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64
L:1485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:1489 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64
L:1489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:1493 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:64
L:1493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:1509 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:65
L:1509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1513 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:65
L:1513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1515 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:65
L:1515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1519 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:65
L:1519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65
L:1545 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66
L:1584 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:68
```

VERIFICATION SUMMARY   DATE: 10/18/2001
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Input Set : **N:\EBONY'S\ES.txt**
Output Set: **N:\CRF3\10182001\I964824.raw**

```
L:1584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68
L:1608 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:69
L:1608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69
L:1624 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:70
L:1624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
```